Amendments to the Claims:

Please amend claims 15, 19, 35, 68, 71 and 74, and add new claims 85-90 as set forth below.

1-14. (Canceled)

15. (Currently amended) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized ACPS, wherein the crystallized ACPS is characterized as being in plate form with space group $P2_1$, and having unit cell parameters of a=76.26Å, b=76.16Å, c=85.69 Å, and beta=93.3°;

(b) obtaining the ~~relative~~ structural coordinates of the crystallized ACPS of step (a), wherein the ~~relative~~ structural coordinates are set forth in Figure 1 and 1A-1 to 1A-107;

(c) generating a three dimensional model of ACPS using the ~~relative~~ structural coordinates of the amino acids of ACPS obtained in step (b), <u>and</u> ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of ACPS from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

16.   (Original) The method of Claim 15, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

17.   (Original)   The method of Claim 16, wherein the agent is an inhibitor of ACPS activity.

18.   (Withdrawn) The method of Claim 16, wherein the agent is an activator of ACPS activity.

19.   (Currently amended) A method for identifying an agent that interacts with an active site of an acyl carrier protein synthase-coenzyme A (ACPS-CoA) complex, comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as being in pyramidal form with space group R3, and having unit cell parameters of a=b=55.82Å and c=92.28Å;

(b) obtaining the ~~relative~~ structural coordinates of the amino acids of the crystallized complex of step (a), wherein the ~~relative~~ structural coordinates are set forth in Figure 2 and 2A-1 to 2A-19;

(c) generating a three dimensional model of ACPS-CoA using the ~~relative~~ structural coordinates of the amino acids obtained in step (b), <u>and</u> ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of the ACPS-CoA complex from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

20.   (Original)   The method of Claim 19, further comprising contacting the identified agent with ACPS-CoA complex in order to determine the effect the agent has on ACPS-CoA complex activity.

241370.2

21. (Original) The method of Claim 20, wherein the agent is an inhibitor of ACPS-CoA complex activity.

22. (Withdrawn) The method of Claim 21, wherein the agent is an activator of ACPS-CoA complex activity.

23-34. (Canceled)

35. (Currently amended) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as being in pyramidal form with space group R3, and having unit cell parameters of a=b=55.82Å and c=92.28Å;

(b) obtaining the ~~relative~~ structural coordinates of the amino acids of the crystallized complex of step (a), wherein the ~~relative~~ structural coordinates are set forth in Figure 2 and 2A-1 to 2A-19;

(c) generating a three dimensional model of ACPS using the ~~relative~~ structural coordinates of the amino acids obtained in step (b), <u>and</u> ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of ACPS from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

36. (Previously presented) The method of Claim 35, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

37. (Previously presented) The method of Claim 36, wherein the agent is an inhibitor of ACPS activity.

38. (Previously presented) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

39. (Previously presented) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of amino acid residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

40. (Previously presented) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a

second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

41. (Previously presented) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63 according to Figure 1 and 1A-1 to 1A-107, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

42. (Previously presented) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

43. (Previously presented) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of amino acid residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

241370.2

44. (Previously presented) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

45. (Previously presented) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63 according to Figure 2 and 2A-1 to 2A-19, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

46. (Previously presented) The method of claim 15, wherein the ± root mean square deviation from the backbone atoms is not more than 1.0 Å.

47. (Previously presented) The method of claim 46, wherein the ± root mean square deviation from the backbone atoms is not more than 0.5 Å.

48. (Previously presented) The method of claim 19, wherein the ± root mean square deviation from the backbone atoms is not more than 1.0 Å.

49. (Previously presented) The method of claim 48, wherein the ± root mean square deviation from the backbone atoms is not more than 0.5 Å.

50. (Previously presented) The method of claim 35, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

51. (Previously presented) The method of claim 50, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

52. (Previously presented) The method of claim 38, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

53. (Previously presented) The method of claim 52, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

54. (Previously presented) The method of claim 39, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

55. (Previously presented) The method of claim 54, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

56. (Previously presented) The method of claim 40, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

57. (Previously presented) The method of claim 56, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

58. (Previously presented) The method of claim 41, wherein the $\pm$ root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

241370.2

59. (Previously presented) The method of claim 58, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

60. (Previously presented) The method of claim 42, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

61. (Previously presented) The method of claim 60, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

62. (Previously presented) The method of claim 43, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

63. (Previously presented) The method of claim 62, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

64. (Previously presented) The method of claim 44, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

65. (Previously presented) The method of claim 64, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

66. (Previously presented) The method of claim 45, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

67. (Previously presented) The method of claim 66, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

68. (Currently amended) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized ACPS, wherein the crystallized ACPS is characterized as being in plate form with space group $P2_1$, and having unit cell parameters of a=76.26Å, b=76.16Å, c=85.69 Å, and beta=93.3°;

(b) obtaining the ~~relative~~ structural coordinates of the crystallized ACPS of step (a);

(c) generating a three dimensional model of ACPS using the ~~relative~~ structural coordinates of the amino acids of ACPS obtained in step (b), <u>and</u> ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of ACPS from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

69. (Previously presented) The method of Claim 68, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

70. (Previously presented) The method of Claim 69, wherein the agent is an inhibitor of ACPS activity.

71. (Currently amended) A method for identifying an agent that interacts with an active site of an acyl carrier protein synthase-coenzyme A (ACPS-CoA) complex, comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as

being in pyramidal form with space group R3, and having unit cell parameters of $a=b=55.82Å$ and $c=92.28Å$;

(b) obtaining the ~~relative~~ structural coordinates of the amino acids of the crystallized complex of step (a);

(c) generating a three dimensional model of ACPS-CoA using the ~~relative~~ structural coordinates of the amino acids obtained in step (b), and ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of the ACPS-CoA complex from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

72. (Previously presented) The method of Claim 71, further comprising contacting the identified agent with ACPS-CoA complex in order to determine the effect the agent has on ACPS-CoA complex activity.

73. (Previously presented) The method of Claim 72, wherein the agent is an inhibitor of ACPS-CoA complex activity.

74. (Currently amended) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as being in pyramidal form with space group R3, and having unit cell parameters of $a=b=55.82Å$ and $c=92.28Å$;

(b) obtaining the ~~relative~~ structural coordinates of the amino acids of the crystallized complex of step (a);

(c) generating a three dimensional model of ACPS using the ~~relative~~ structural coordinates of the amino acids obtained in step (b), <u>and</u> ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of ACPS from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

75. (Previously presented) The method of Claim 74, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

76. (Previously presented) The method of Claim 75, wherein the agent is an inhibitor of ACPS activity.

77. (Previously presented) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

78. (Previously presented) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second

monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

79. (Previously presented) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

80. (Previously presented) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

81. (Previously presented) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

82. (Previously presented) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues

ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

83. (Previously presented) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

84. (Previously presented) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

85. (New) The method of claim 15, wherein ACPS is cloned and isolated from *B. subtilis*.

86. (New) The method of claim 19, wherein ACPS is cloned and isolated from *B. subtilis*.

87. (New) The method of claim 35, wherein ACPS is cloned and isolated from *B. subtilis*.

88. (New) The method of claim 68, wherein ACPS is cloned and isolated from *B. subtilis*.

89. (New) The method of claim 71, wherein ACPS is cloned and isolated from *B. subtilis*.

90. (New) The method of claim 74, wherein ACPS is cloned and isolated from *B. subtilis*.